

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1. - 63. (Canceled)

64. (Withdrawn- currently amended) The fragment complementation system of claim ~~63~~ 78, wherein said first oligopeptide and said second oligopeptide comprise a signal peptide that translocates said first oligopeptide and said second oligopeptide through the plasma membrane of a host cell in which said first oligopeptide and said second oligopeptide are expressed.

65. (Canceled)

66. (Currently amended) The fragment complementation system of claim ~~63~~ 79, wherein said ~~Class A~~ TEM-1 β -lactamase protein comprises amino acids 26 to 288 of the following sequence:

His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly
26				30					35					40	
Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu
			45					50					55		
Glu	Ser	Phe	Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys
		60					65					70			
Val	Leu	Leu	Cys	Gly	Ala	Val	Leu	Ser	Arg	Ile	Asp	Ala	Gly	Gln	Glu
	75					80				85					
Gln	Leu	Gly	Arg	Arg	Ile	His	Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr
90				95					100				105		
Ser	Pro	Val	Thr	Glu	Lys	His	Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu
				110					115				120		

Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
125 130 135
Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
140 145 150
Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
155 160 165
Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Val Ala
170 175 180 185
Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu
190 195 200
Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala
205 210 215
Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp
220 225 230
Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu
235 240 245
Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly
250 255 260 265
Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly
270 275 280
Ala Ser Leu Ile Lys His Trp
285

(SEQ ID NO:2);

~~wherein said first and second break point is between amino acid residues Glu 197~~
and Leu 198.

67. (Canceled).

68. (Withdrawn-Currently amended) The fragment complementation system of claim ~~63~~ 78, wherein said fragment complementation system further comprises a first peptide that enhances the functional reconstitution of said N-terminal fragment and said C-terminal fragment in comparison with the identical system without said first peptide, wherein said first peptide is 3-12 amino acids in length.

69. (Withdrawn-Previously Presented) The fragment complementation system of claim 68, wherein said first peptide is 3 amino acids in length.

70. (Withdrawn-Previously Presented) The fragment complementation system of claim 69, wherein said first peptide is covalently bonded to the active site of a thioredoxin protein, wherein the sequence of said first peptide is GRE.

71. (Currently amended) The fragment complementation system of claim ~~63~~ 78, wherein
said first polypeptide linker is 3-30 amino acids in length; and
wherein said second polypeptide linker is 3-30 amino acids in length.

72. (Currently amended) The fragment complementation system of claim 71, further comprising a first complementation enhancement peptide fused between the N-terminal fragment of the ~~Class A~~ TEM-1 β -lactamase protein and the first polypeptide linker; and

a second complementation enhancement peptide fused between the C-terminal fragment of the ~~Class A~~ TEM-1 β -lactamase protein and the second polypeptide linker.

73. (Previously Presented) The fragment complementation system of claim 72, wherein
the sequence of said first complementation enhancement peptide is selected from the group consisting of HSE, GRE, EKR, and NGR, and
the sequence of said second complementation enhancement peptide is selected from the group consisting of REQ, QGN, DGR, GRR and GNS.

74. (Previously presented) The fragment complementation system of claim 73, wherein
the sequence of said first complementation enhancement peptide is HSE, and the sequence of said second complementation enhancement peptide is REQ.

75. (Previously presented) The fragment complementation system of claim 73, wherein the sequence of said first complementation enhancement peptide is NGR, and the sequence of said second complementation enhancement peptide is QGN or GNS.

76. (Previously presented) The fragment complementation system of claim 73, wherein the sequence of said first complementation enhancement peptide is GRE, and the sequence of said second complementation enhancement peptide is DGR.

77. (Previously presented) The fragment complementation system of claim 73, wherein the sequence of said first complementation enhancement peptide is EKR, and the sequence of said second complementation enhancement peptide is GRR.

78 (New) A fragment complementation system, said system comprising a first oligopeptide sequence and a second oligopeptide sequence;
wherein said first oligopeptide sequence is a fusion protein comprising, in the direction of translation, an N-terminal fragment of a TEM-1 β -lactamase protein, not less than 25 amino acids in length, fused through a C-terminal residue to a first flexible polypeptide linker and a first interactor domain; and

wherein said second oligopeptide sequence is a fusion protein comprising, in the direction of translation, a second interactor domain, a second flexible polypeptide linker fused through an N-terminal residue to a C-terminal fragment of the TEM-1 β -lactamase protein, not less than 25 amino acids in length;

wherein said C-terminal residue and N-terminal residue are located in a solvent exposed loop between amino acid residues Thr 195 and Ala 202 of the TEM-1 β -lactamase protein and,

wherein upon binding of said first interactor domain with said second interactor domain, said N-terminal fragment and said C-terminal fragment reconstitute to form a functional TEM-1 β -lactamase protein.

79. (New) The fragment complementation system of claim 78, wherein the C-terminal residue of the N-terminal fragment is Glu 197, and the C-terminal residue of the N-terminal fragment is Leu 198.